human CAP-1

MLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVSIPRDIMLEELSHLSNRGARLFKM 60

RQRRSDKYTFENFQYQSRAQINHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNP 120

DNIAPGYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPKLFKPEGKAELP 180

DYRSFNRVATPFGGFEKASRMVKFKVPDFELLLLTDPRFMSFVNPLSGRRSFNRTPKGWI 240

SENIPVITTEPTDDTTVPESEDL

FIG. 1A

mouse CAP-1

MLSHSAMVKQRKQQASAITKEIHGHDVDGMDLGKKVSIPRDIMIEELSHFSNRGARLFKM 60

RQRRSDKYTFENFQYESRAQINHNIAMQNGRVDGSNLEGGSQQGPSTPPNTPDPRSPPNP 120

ENIAPGYSGPLKEIPPERFNTTAVPKYYRSPWEQAIGSDPELLEALYPKLFKPEGKAELR 180

DYRSFNRVATPFGGFEKASKMVKFKVPDFELLLLTDPRFLAFANPLSGRRCFNRAPKGWV 240

SENIPVVITTEPTEDATVPESDDL

FIG. 1B

human CAP-2

```
                                                           60
MPLSGTPAPNKKRKSSKLIMELTGGGQESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF
                                                          120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
                                                          180
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGETGSGDQAGGEGKHITV
                                                          240
FKTYISPWERAMGVDPQQKMELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTF

QMPKFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEPVDYNVDIGIPLDGETEEL
```

FIG. 1C

mouse CAP-2

```
                                                           60
MPLSGTPAPNKKRKSSKLIMELTGGGRESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF
                                                          120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLETAGQGFSYGKGSSGGQAGSSG
                                                          180
SAGQYGSDRHQQGSGFGAGGSGGPGGQAGGGGAPGTVGLGEPGSGDQAGGDGKHVTVFKT
                                                          240
YISPWDRAMGVDPQQKVELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMP

KFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEHVDYNVDVGIPLDGETEEL
```

FIG. 1D

FIG. 1E

human CAP-1

```
         10        20        30        40        50        60        70        80        90       100
GTCCCAGGTTCAAGGATAAAAACCATCAGGCCCAAGTGCCATCCATAGTCCATCTCCAGAGTCTTCCTCCACAAACTGGGATTCATCCCCGCTGAAAAAG
CAGGGTCCAAGTTCCTATTTTTGGTAGTCCGGGTTCACGGTAGGTATCAGGTAGAGGTCTCAGAAGGAGGTGTTTGACCCTAAGTAGGGGCGACTTTTTC

        110       120       130       140       150       160       170       180       190       200
CACAATCTAACAGCAAGGGAACAAAAAAACCATGCTATCACATAATACTATGATGAAGCAGAGAAAACAGCAAGCAACAGCCATCATGAAGGAAGTCCAT
GTGTTAGATTGTCGTTCCCTTGTTTTTTTGGTACGATAGTGTATTATGATACTACTTCGTCTCTTTTGTCGTTCGTTGTCGGTAGTACTTCCTTCAGGTA

        210       220       230       240       250       260       270       280       290       300
GGAAATGATGTTGATGGCATGGACCTGGGCAAAAAGGTCAGCATCCCCAGAGACATCATGTTGCAAGAATTATCCCATCTCACTAACCGTGGTGCCAGGC
CCTTTACTACAACTACCGTACCTGGACCCGTTTTTCCAGTCGTAGGGGTCTCTGTAGTACAACGTTCTTAATAGGGTAGAGTGATTGGCACCACGGTCCG

        310       320       330       340       350       360       370       380       390       400
TATTTAAGATGCGTCAAAGAAGATCTCACAAATACACATTTGAAAATTTCCAGTATCAATCTAGAGCACAAATAAATCACAGTATTGCTATGCAGAATGG
ATAAATTCTACGCAGTTTCTTCTAGAGTGTTTATGTGTAAACTTTTAAAGGTCATAGTTAGATCTCGTGTTTATTTAGTGTCATAACGATACGTCTTACC

        410       420       430       440       450       460       470       480       490       500
GAAAGTGGATGGAAGTAACTTGGAAGGTGGTTCGCAGCAAGCCCCCTTGACTCCTCCCAACACCCCAGATCCACGAAGCCCTCCAAATCCAGACAACATT
CTTTCACCTACCTTCATTGAACCTTCCACCAAGCGTCGTTCGGGGGAACTGAGGAGGGTTGTGGGGTCTAGGTGCTTCGGGAGGTTTAGGTCTGTTGTAA

        510       520       530       540       550       560       570       580       590       600
GCTCCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAAATTCAACACCACAGCTGTCCCTAAGTACTATCAATCTCCCTGGGAGCAAGCCATTA
CGAGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTTTAAGTTGTGGTGTCGACAGGGATTCATGATAGTTAGAGGGACCCTCGTTCGGTAAT

        610       620       630       640       650       660       670       680       690       700
GCAATCATCCGGAGCTTTTAGAGGCTTTATATCCTAAACTTTTCAAGCCTGAAGGAAAGGCAGAACTGCCTGATTACAGGAGCTTTAACAGGGTTGCCAC
CGTTACTAGGCCTCGAAAATCTCCGAAATATAGGATTTGAAAAGTTCGGACTTCCTTTCCGTCTTGACGGACTAATGTCCTCGAAATTGTCCCAACGGTG

        710       720       730       740       750       760       770       780       790       800
ACCATTTGGAGGTTTTGAAAAAGCATCAAGAATGGTTAAAATTTAAAGTTCCAGATTTTGAGCTACTATTGCTAACAGATCCCAGGTTTATGTCCTTGTC
TGGTAAACCTCCAAAACTTTTTCGTAGTTCTTACCAATTTAAATTTCAAGGTCTAAAACTCGATGATAACGATTGTCTAGGGTCCAAATACAGGAAACAG

        810       820       830       840       850       860       870       880       890       900
AATCCCCTTTCTGGCACGACGTCCTTTAATAGGACTCCTAAGGGATGGGATATCTGAGAATATTCCTATAGTGATAACAACCGAACCTACAGATGATACCA
TTAGGGGAAAGACCGTCTGCCAGGAAAATTATCCTGAGGATTCCCTACCTATAGACTCTTATAAGGATATCACTATTGTTGGCTTGGATGTCTACTATGGT

        910       920       930       940       950       960       970       980       990      1000
CTGTACCAGAATCAGAAGACCTATGAAAAGAAAGTTGTATGTGCCACATAAAACTCTGAATATAAAAGTTGCTGTTCTACTATTTTAACTACTGGCAAAG
GACATGGTCTTAGTCTTCTGGATACTTTTCTTTCAACATACACGGTGTATTTTGAGACTTATATTTTCAACGACAAGATGATAAAATTGATGACCGTTTC

       1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
CACTTGCATTTTTCATTAGTAGCAACAATAGCAATTTAGTGAATTTTCTGACATTCAATTTCAATCTCAGATCAAATACTAATAAACAATTAGAA
GTGAACGTAAAAAGTAATCATCGTTGTTATCGTTAAATCACTAAAAGGAAAAGACTGTAAGTTAAAGTTAGAGTCTAGTTTATGATTATTTGTTAATCTT

       1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
ATCTTACTTTAAAAAACTTATAACTCACTGTCTTCATCATAATTTGTTTTCACCTGGTTTAAAGAATCCAGATATTTTACTGCAAAAGTTCAGATGG
TAGAATGAAATTTTTTGAATATTCAGTGAACAGAAGTAAGTATTAAAACAAAAGTGGACCAAATTTCTTAGGTCTATAAAATGACGTTTTCAAGTCTACC

       1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
AAAAGTAATTGACAGCTTCACCTTTGTCTCATTTTATATGATTTATTACAGTGTAAGTTTTCAAGTGGAATCTAGAATCAAAATACAGGGAGAGATATG
TTTTCATTAACTGTCGAAGTGGAAACAGAGTAAAATATACTAAATAATGTCACATTCAAAAAGTTCACCTTAGATCTTAGTTTTATGTCCCTCTCTATAC

       1310      1320      1330      1340      1350      1360      1370      1380      1390      1400
AAGACCTATTCAGAGTTTCATCTGGGGATGAAAGCTATGGAAGATGATGTACAAAATGTTATTGATGGGAGAAAATGGTTGGTGTGTCCTTTCTGGTGACCA
TTCTGGATAAGTCTCAAAGTAGACCCCTACTTTCGATACCTTCTACTACATGTTTACAATAACTACCTCTTTTACCAACCACACAGGAAAGACCACTGGT

       1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
TGACAAAAATAATATGTCTTGATGAAGTCTTTTCATTAGTACACTCTTAGAATTCTAAAGTGCTTTGCACTTTTCAATATGTTTTGAATCATTAGGTAAATTT
ACTCTTTTATTATACAGAACTACTTCAGAAAAGTAATCAGTGAGAATCTTAAGATTTCACGAAACGTGAAAAGTTATACAAAACTTAGTAATCCATTAAA

       1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
ATTCTGCATGATATTCTCCAAAATTCAATTCAGTTATTATATTCATTTAGCATTAAGTCAAGGAGACTGAGAATGACTCAAGGGACGTCATAGTACCATA
TAAGACCTACTATAAGAGGTTTTAAGTTAAGTCAATAATAATAAGTAAATCGTAATTCAGTTCCTCTGACTCTTACTGAGTTCCCTGCAGTATCATGGTAT

       1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
GTTTTAAGGACCAAGGTGTGCCCAGAATTCAAGTTTCACAAATCCCAATGCGTGTCATTGATTATGTTCAACTTTATGTGTGCATTCTTAGAAGAGTAAG
CAAAATTCCTGGTTCCACACGGGTCTTAAGTTCAAAGTGTTTAGGGTTACGACACGTAACTAATACAAGTTGAAATACACACGTTAGAATCTTCTCATTC

       1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
AACAAATAAAGTACACCGTAATATACATATAAATACATTCATGTTTGTCAGACAAGGAAAGAGTAAGTAATTTGAATTGGCAGCTTTCTTTGCTAAATCT
TTGTTTATTTCATGTGGCATTATATGTATATTTATGTAAGTACAAACAGTCTGTTCCTTTCTCATTCATTAAACTTAACCGTCGAAAGAAACGATTTAGA

       1810      1820      1830      1840      1850      1860      1870      1880      1890      1900
TTAAATTCTGTTAAGATCCTCAAGTAACTGGGGAGTACATGCTTTAGGACACAAACAAAAACAAAGGGCATGAAAGTATCTGAAAGCAATGTAGCACATA
AATTTAAGACAATTCTAGGAGTTCATTGACCCCTCATGTACGAAATCCTGTGTTTGTTTTTGTTCCCGTACTTTCATAGACTTTCGTACATCGTGTAT

       1910      1920      1930      1940      1950      1960      1970      1980      1990      2000
TCTATCGTAATATATGTAATATATTGACATAAAAGACACAAACTAATAAAGTTATAGTTATATCTTAAAATATAATTCAAGAAGCATATGACATATAA
AGATAGCATTATATACATTATATAACTGTATTTTCTGTGTTTGATTATATTCAATATCAATATAGAATTTTATATTAACTTCTTCGTATACTGTATATT

       2010      2020      2030      2040      2050      2060      2070      2080      2090      2100
CTTATAGAAATCAGTATCAATTCCTCCCATTTCAATTCAGTTAAGACTTCTGTCGATAGATGTTTATAGCAGAGAAGAAATGTCTCATCAATAGCAAAACT
GAATATCTTTAGTCATAGTTAAGGAGGGTAAAGTTAAGTCAATTCTGAAGACACTATCTACAAATATCGTCTCTTCTTTACGAGTAGTTATCGTTTTGA

       2110      2120      2130      2140      2150      2160      2170      2180      2190      2200
ATCAGATAAAGTTTAGGAGATAGGAAGAAGGACTGTGTGTAGTAATGAAAATACCAAGTTGCAACATTACATGTTTACAAAAAAAATCTGTGTTTGTAGT
TAGTCTATTTCAAATCCTCTATCCTTCTTCCTGACACACATCATTACTTTATGGTTCAACGTTGTAATGTACAAATGTTTTTTTTTAGACACAAACATCA

       2210      2220      2230      2240      2250      2260      2270      2280      2290      2300
GTGCAAGTTGGTGACTGTTTTAATCATCATCTAGACTTGTTAAGTAGAAAAATTTTAAAAATTTGCTTATGAAAATATAAACCCCCAGAAAGTAACAATGA
CACCTTCAACCACTGACAAAATTAGTAGTAGATCTGAACAATTCATCTTTTTAAAATTTTAAACGAATACTTTTATATTGGGGGTCTTTCATTGTTACT

       2310      2320      2330      2340      2350      2360      2370      2380      2390      2400
CAAAGTAATTAATTTATATATATTATTGTAGAGAATTTGTATATTTTTAAAGATGTCTTAACATATCTTAATTTTATTATTTATAAGTTTTGGTGTTTACCTG
GTTTCATTAATTAAATATATATAATAACATCTCTTAAACATATAAAAAATTTCTACAGAATTCTTATAGAATTAAAATAAATATTCAAAACCACAAATGGAC

       2410      2420      2430      2440      2450      2460      2470      2480      2490      2500
TTTTAAAATGATAATGTTGGCATCTGTGATAAACTATCAATCAGGCTCCCATCATGCCCATTTTTGTTCATTTTAATCTTTAAAAAATAAAAATTAGGCA
AAAATTTTACTAATTACAACCGTAGACACTATTTGATAGTTAGTCCGAGGGTAGTACGGTAAAAACAAGTAAAATTAGAAATTTTTTTATTTTTAATCCGT

       2510      2520      2530
TATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ATAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
```

FIG. 2A

mouse CAP-1

```
        10        20        30        40        50        60        70        80        90       100
ATTCGGCACATGGCATCGAGGGACCATGCCGTTCCAGGTTCAAGGATAAAACCCATTGGGCCATAGTGCCGTCATATTCCACCTTCAGTGCCTTCCTCCA
TAAGCCGTGTACCCTAGCTCCCTGGTACGGCAAGGTCCAAGTTCCTATTTTGGGTAACCCGGTATCACGGCAGTATAAGGTGGAAGTCACGGAAGGAGGT


       110       120       130       140       150       160       170       180       190       200
CAATTGGGATTCACCCCTGCTGAAAAGCCGCACGCTGACAGCAAGGGAACAAAAAACTATGCTATCACATAGTGCCATGGTGAAGCAAAGGAAACAGCAAG
GTTAACCCTAAGTGGGGACGACTTTTCGCGTGCGACTGTCGTTCCCTTGTTTTTTGATACGATAGTGTATCACGGTACCACTTCGTTTCCTTTGTCGTTC


       210       220       230       240       250       260       270       280       290       300
CATCAGCCATCACGAAGGAAATCCATGGACATGATGTTGACGGCATGGACCTGGGCAAAAAAGTTAGCATCCCCAGAGACATCATGATAGAAGAATTGTC
GTAGTCGGTAGTGCTTCCTTTAGGTACCTGTACTACAACTGCCGTACCTGGACCCGTTTTTTCAATCGTAGGGGTCTCTGTAGTACTATCTTCTTAACAG


       310       320       330       340       350       360       370       380       390       400
CCATTTCAGTAATCGTGGGGCCAGGCTGTTTAACATGCGTCAAAGAAGATCTGACAAATACACCTTTGAAAATTTCCAGTATGAATCTAGAGCACAAATT
GGTAAAGTCATTAGCACCCCGGTCCGACAAATTCTACGCAGTTTCTTCTAGACTGTTTATGTGGAAACTTTTAAAGGTCATACTTAGATCTCGTGTTTAA


       410       420       430       440       450       460       470       480       490       500
AATCACAATATCGCCATGCAGAATGGGAGAGTTGATGGAAGCAACCTGGAAGGTGGCTCACAGCAAGGCCCCTCAACTCCGCCCAACACCCCCGATCCAC
TTAGTGTTATAGCGGTACGTCTTACCCTCTCAACTACCTTCGTTGGACCTTCCACCGAGTGTCGTTCCGGGGAGTTGAGGCGGGTTGTGGGGGCTAGGTG


       510       520       530       540       550       560       570       580       590       600
GAAGCCCCCCAAATCCAGAGAACATCGCACCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAGGTTTAACACGACGGCCGTTCCTAAGTACTA
CTTCGGGGGCGTTTAGGTCTCTTGTAGCGTGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTCCAAATTGTGCTGCCGGCAAGGATTCATGAT


       610       620       630       640       650       660       670       680       690       700
CCGGTCTCCATGGGAGCAGGCGATTGGCAGCGATCCGGAGCTCCTGGAGGCTTTGTACCCAAAACTTTTCAAGCCTGAAGGAAAAGCAGAACTGCGGGAT
GGCCAGAGGTACCCTCGTCCGCTAACCGTCGCTAGGCCTCGAGGACCTCCGAAACATGGGTTTTGAAAAGTTCGGACTTCCTTTTCGTCTTGACGCCCTA


       710       720       730       740       750       760       770       780       790       800
TACAGGAGCTTTAACAGGGTTGCCACTCCATTTGGAGGTTTTGAAAAAGCATCAAAAATGGTCAAATTCAAAGTTCCAGATTTTGAACTACTGCTGCTGA
ATGTCCTCGAAATTGTCCCAACGGTGAGGTAAACCTCCAAAACTTTTTCGTAGTTTTTACCAGTTTAAGTTTCAAGGTCTAAAACTTGATGACGACGACT


       810       820       830       840       850       860       870       880       890       900
CAGATCCCAGGTTCTTGGCCTTTGCCAATCCTCTTTCGGGCAGACGATGCTTTAACAGGGCGCCAAAGGGGTGGGTATCTGAGAATATCCCCGTCGTCAT
GTCTAGGGTCCAAGAACCGGAAACGGTTAGGAGAAAGCCCGTCTGCTACGAAATTGTCCCGCGGTTTCCCCACCCATAGACTCTTATAGGGGCAGCACTA


       910       920       930       940       950       960       970       980
CACAACTCAGCCTACAGAAGACGCCACTGTACCGGAATCAGATGACCTGTGAGAGGGAAGCTGGGCATGCCACAGGAAGTTC
GTGTTGACTCGGATGTCTTCTGCGGTGACATGGCCTTAGTCTACTGGACACTCTCCCTTCGACCCCTACGGTGTCCTTCAAG
```

FIG. 2B

human CAP-2

```
                                                                                    100
CGGTCACAGC AGCTCAGTCC TCCAAAGCTG CTGGACCCCA GGGAGAGCTG ACCACTGCCC GAGCAGCCGG CTGAATCCAC CTCCACAATG CCGCTCTCAG
                                                                                    200
GAACCCCGGC CCCTAATAAG AAGAGGAAAT CCAGCAAGCT GATCATGGAA CTCACTGGAG GTGGACAGCA GAGCTCAGGC TTCAACCTGG GCAAAAAGAT
                                                                                    300
CAGTGTCCCA AGGGATGTGCA TGTTGGAGGA ACTGTCGCTG CTTACCAACC GGGGCTCCAA GATGTTCAAA CTGCGGCAGA TGAGGGTGGA GAAGTTTATT
                                                                                    400
TATGAGAACC ACCCTGATGT TTTCTCTGAC AGCTCAATGG ATCACTTCCA GAAGTTCCTT CCAACAGTGG GGGCACAGCT GGGCACAGCT CGTCAGGGAT
                                                                                    500
TCTCATACAG CAAGAGCAAC GGCAGAGGCG GCAGCCAGGC AGGGGGCAGT GGCTCTGCCG GACAGTATGG CTCTGATCAG CAGCACCATC TGGGCTCTGG
                                                                                    600
GTCTGGAGCT GGGGGTACAG GTGGTCCCGC GGGCCAGGCT GGCAGAGGAG GAGCTGCTGG CACACAGGGG GTTGGTGAGA CAGGATCAGG AGACCAGGCA
                                                                                    700
GGCGGAGAAG GAAAACATAT CACTGTGTTC AAGACCTATA TTTCCCCATG GGAGCGAGCC ATGGGGGTTG ACCCCCAGCA AAAAATGGAA CTTGGCATTG
                                                                                    800
ACCTGCTGGC CTATGGGGCC AAAGCTGAAC TTCCCAAATA TAAGTCCTTC AACAGGACGG CAATGCCCTA TGGTGGATAT GAGAAGGCCT CCAAACGCAT
                                                                                    900
GACCTTCCAG ATGCCCAAGT TTGACCTGGG GCCCTTGCTG AGTGAACCCC TGGTCCTCTA CAACCAAAAC CTCTCCAACA GGCCTTCTTT CAATCGAACC
                                                                                    1000
CCTATTCCCT GGCTGAGCTC TGGGGAGCCT GTAGACTACA ACGTGGATAT TGGCATCCCC TTGGATGGAG AAACAGAGGA GCTGTGAGGT GTTTCCTCCT
CTGATTTGCA TCATTTCCCC TCTCTGGCTC CAATTTGGAG A
```

FIG. 2C

mouse CAP-2

```
                                                                              100
GCCGGGGAGA GCCGACCACC AACTGAGCAG CTGGTCAGAT CCACCTCCAC CATGCCACGC TCAGGAACCC CGGCCCCTAA CAAGAGGAGG AAGTCAAGCA
                                                                              200
AACTGATTAT GGAGCTCACT GGAGGTGGCC GGGAGAGCTC AGGCCTGAAC CTGGGCAAGA AGATCAGTGT CCCAAGGGAT GTGATGTTGG AGGCAGCTGTC
                                                                              300
CCTTCTTACC AACCGAGGCT CCAAGATGTT CAAGCTACGG CAGATGCGGG TGGAGAAATT TATCTATGAG AATCACCCCG ATGTTTTCTC TGACAGCTCA
                                                                              400
ATGGATCACT TCCAGAAGTT TCTTCCCACA GTGGGAGGAC AGCTGGACAC AGCTGGTCAG GGCTTCTCAT ATGGCAAGGG CAGCAGTGGA GGCCAGGCTG
                                                                              500
GCAGCAGTGG CTCTGCTGGA CAGTATGGCT CTGACCGTCA TCAGCAGGGC TCTGGGTTTG GAGCTGGGGG TTCAGGTGGT CCTGGGGGCC AGGCTGGTGG
                                                                              600
AGGCAGGAGCT CCTGGCACAG TAGGGCTTGG AGAGCCCGGA TCAGGTGACC AGGCAGGTCG AGATGGAAAA CATGTCACTG TGTTCAAGAC TTATATTTCC
                                                                              700
CCATGGGATC GGGCCATGGG GGTTGATCCT CAGCAAAAAG TGGAACTTGG CATTGACCTA CTGGCATACG GTGCCAAAGC TGAACTCCCC AAATATAAGT
                                                                              800
CCTTCAACAG GACAGCAATG CCCTACGGTG GATATGAGAA GGCCTCCAAA CGCATGACCT TCCAGATGCC CAAGTTTGAC CTGGGGCCTC TGCTGAGTGCA
                                                                              900
ACCCCTGGTC CTCTACAACC AGAACCTCTC CAACAGGCCT TCTTTCAATC GAACCCCTAT TCCCTGGTTG AGCTCTGGGG AGCATGTAGA CTACAACGTG
                                                                              1000
GATGTTGGTA TCCCCTTGGA TGGAGAGACA GAGGAGCTGT GAAGTGCCTC CTCCTGTCAT GTGCATCATT TCCCTTCTCT GGTTCCAATT TGAGAGTGGA
                                                                              1100
TGCTGGACAG GATGCCCCAA CTGTTAATCC AGTATTCTTG TGGCAATGGA GGGTAAAGGG TGGGGTCCGT TGCCTTTCCA CCCTTCAAGT TCCTGCTCCG
AAGCATCCCT CCTCACCAGC TCAGAGCTCC CATCCTGCTG TACCATATGG AATCTGCTCT TTTATGGAAT TTTCT
```

FIG. 2D

FIG. 3

FIG. 4C

Calsarcin-1

Calsarcin-2

GM | DM
1 2 3 5

Calsarcin-1

Calsarcin-2

GAPDH

FIG. 4E

FIG. 4A

E9.5   E12.5   E15.5

Calsarcin-1

Calsarcin-2

Heart   Gastroc   Soleus   Liver

Calsarcin-1

Tubulin
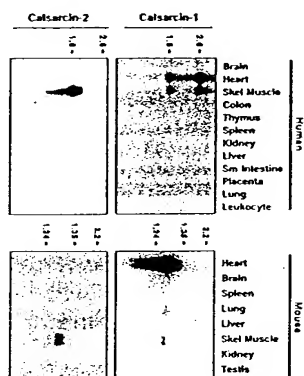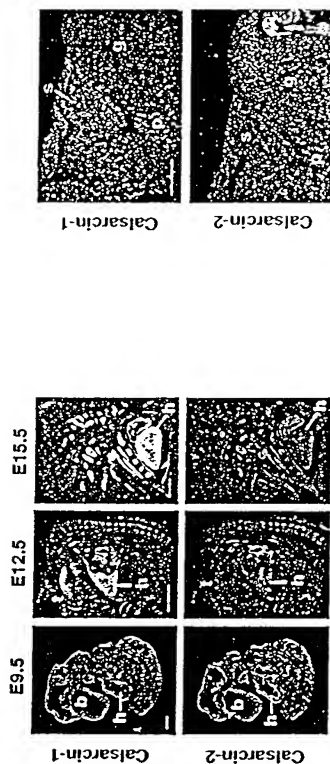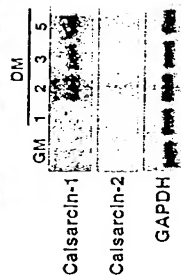
FIG. 4D

Calsarcin-1

FIG. 4B
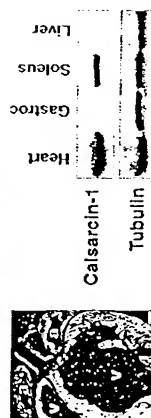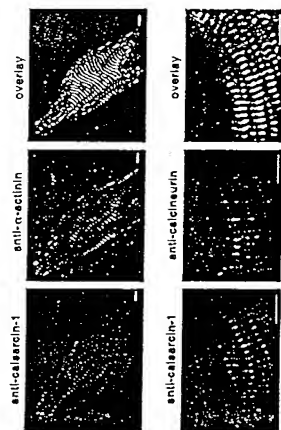
FIG. 5A

FIG. 5B

FIG. 6A

FIG. 6B

FIG. 6C

FIG. 7
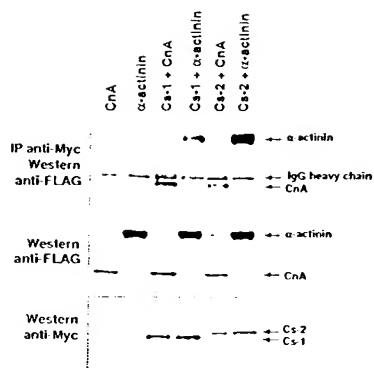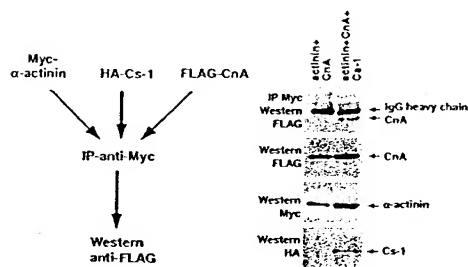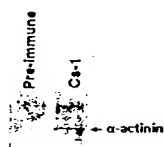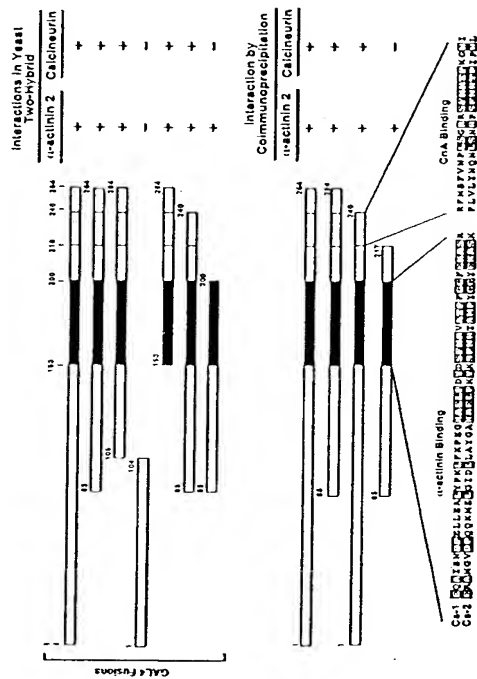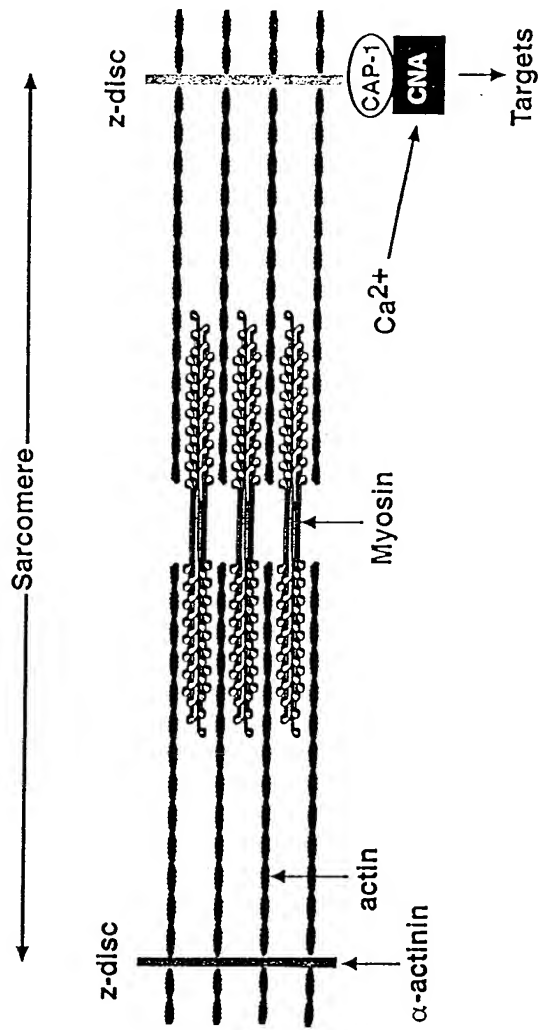
FIG. 8
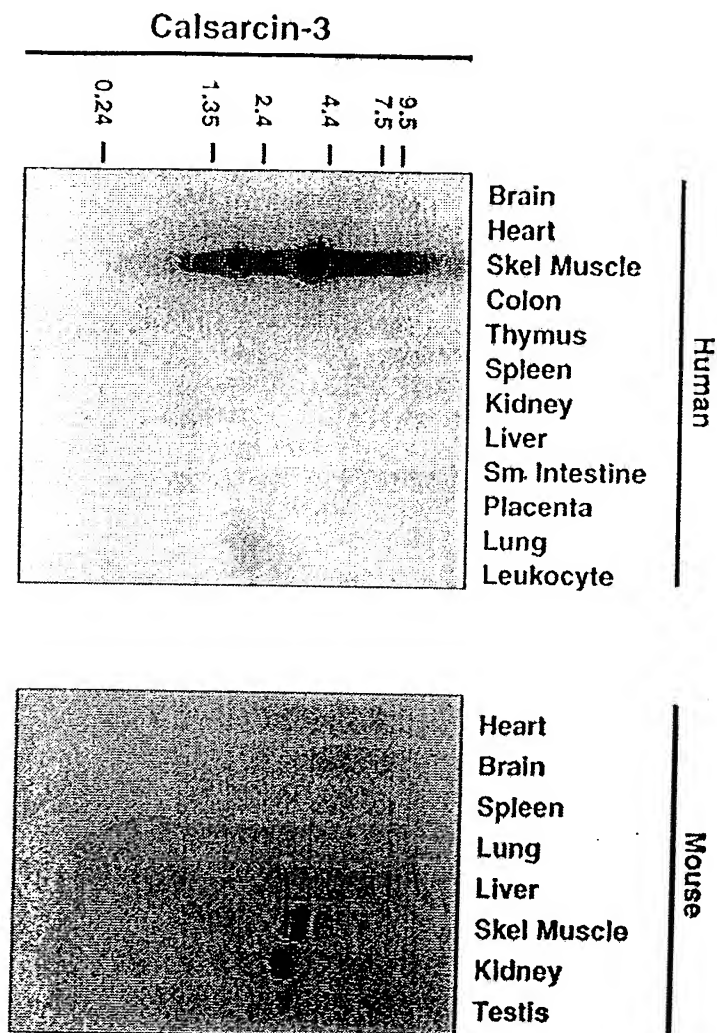
FIG. 9
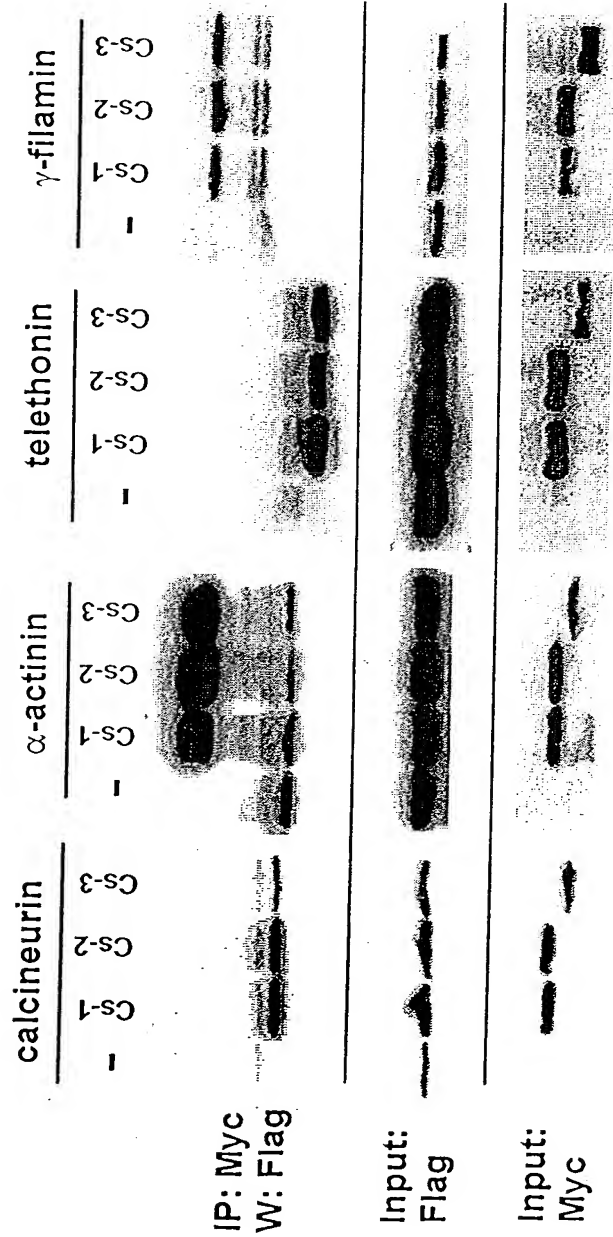
FIG. 10

calsarcin-3   actinin   merge
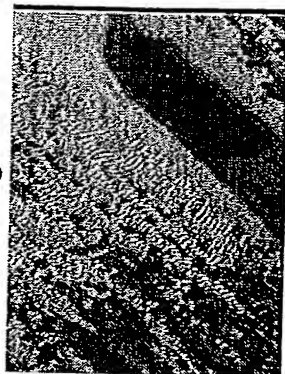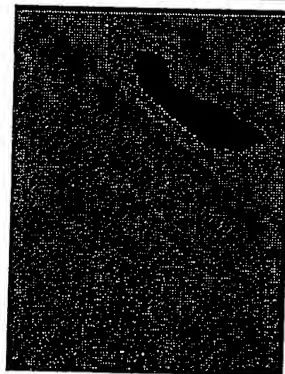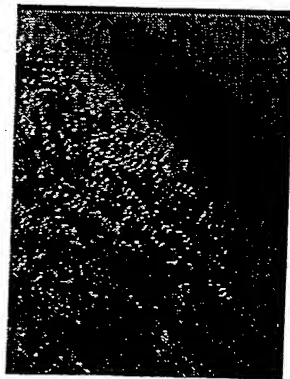
FIG. 11

FIG. 12
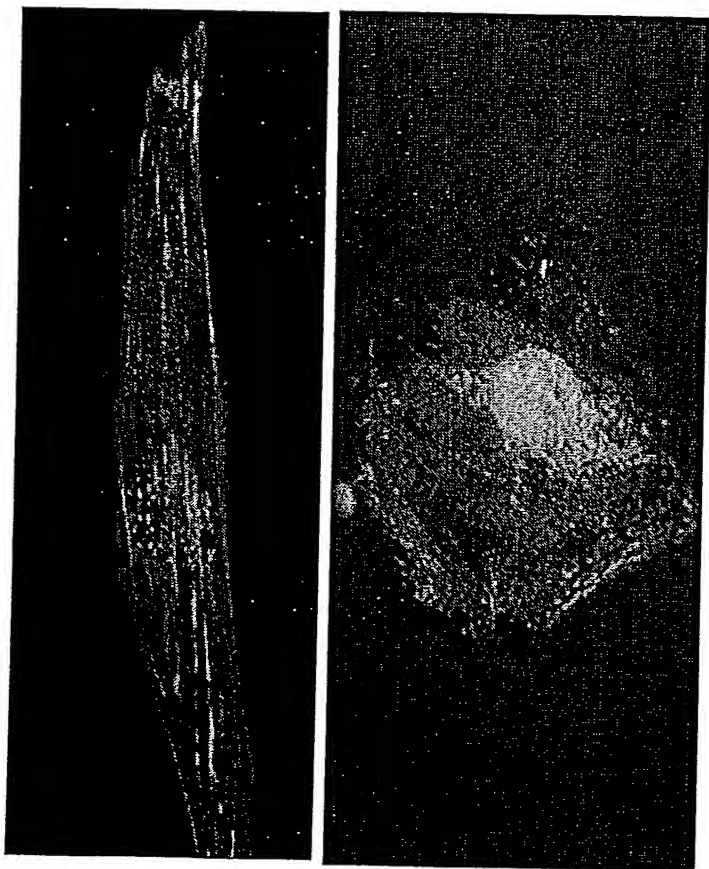
ClustalW Formatted Alignments

calsarcin-3
calsarcin-2
calsarcin-1

FIG. 13